

Exhibit A  
Comparison of the Amino Acid Sequences of  
SEQ ID NO:24 and NP\_660187

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaGAABJayWj: 1219 aa

>seqid24

vs /tmp/fastaHAACJayWj library

searching /tmp/fastaHAACJayWj library

1344 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 40, opt: 28, gap-pen: -12/ -2, width: 16

Scan time: 0.034

The best scores are:

NP\_660187 ACCESSION:NP\_660187 NID: gi 21729876 re (1344) 4838 opt

>>NP\_660187 ACCESSION:NP\_660187 NID: gi 21729876 ref NP\_ (1344 aa)

initn: 7156 initl: 4838 opt: 4838

Smith-Waterman score: 7274; 85.311% identity in 1382 aa overlap (1-1219:1-1344)

	10	20	30	40	50	60
seqid2	MTRKRTYWPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					
	.....					
NP_660	MTRKRTYWPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					
	10	20	30	40	50	60
	70	80	90	100	110	120
seqid2	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					
	.....					
NP_660	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
seqid2	SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTLIFDALLGICFCIASVLG					
	.....					
NP_660	SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTLIFDALLGICFCIASVLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
seqid2	PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFQAAVSS					
	.....					
NP_660	PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSS					
	190	200	210	220	230	240
	250	260	270	280	290	300
seqid2	FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIG					
	.....					
NP_660	FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIG					
	250	260	270	280	290	300
	310	320	330	340	350	360
seqid2	YTAFAIILCYLLVFPLEVFMTMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP					

[illegible]

```

NP_660 NKVFRCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSP
      910      920      930      940      950      960

      800      810      820      830      840      850
seqid2 YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPFLFSHILNSLQGLSSIHVYGKTED
      .....
NP_660 YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPFLFSHILNSLQGLSSIHVYGKTED
      970      980      990     1000     1010     1020

      860      870      880      890      900      910
seqid2 FISQFKRLTDAQNNYLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
      .....
NP_660 FISQFKRLTDAQNNYLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
      1030     1040     1050     1060     1070     1080

      920      930      940      950      960      970
seqid2 VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
      .....
NP_660 VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
      1090     1100     1110     1120     1130     1140

      980      990     1000     1010     1020     1030
seqid2 IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
      .....
NP_660 IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
      1150     1160     1170     1180     1190     1200

      1040     1050     1060     1070     1080     1090
seqid2 IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKEI
      .....
NP_660 IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKEI
      1210     1220     1230     1240     1250     1260

      1100     1110     1120     1130     1140     1150
seqid2 SKFPPKLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTI
      .....
NP_660 -----ILIDEATASIDMETDTLIQRTI
      1270     1280

      1160     1170     1180     1190     1200     1210
seqid2 REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
      .....
NP_660 REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
      1290     1300     1310     1320     1330     1340

seqid2 LR
      ::
NP_660 LR

```